

| Isolate | Short-reads coverage | Long-reads coverage | Number of contigs <sup>a</sup> | N50 <sup>a</sup> (bp) | Number of chromosome-associated contigs <sup>b</sup> | Length of chromosome-associated contigs (bp) | Number of plasmid-associated contigs <sup>b</sup> | Length of plasmid-associated contigs (bp)                              | Undefined contigs <sup>c</sup> | Genome closed | Inferred localization of <i>pmrCAB</i> |
|---------|----------------------|---------------------|--------------------------------|-----------------------|--|--|---|--|--------------------------------|---------------|--|
| 67659   | 116.096              | 70.689              | 6                              | 4,174,758             | 1  | 4,174,758                                    | 3   | 120,650 <sup>d</sup> ;<br>40,936 <sup>d</sup> ;<br>16,673 <sup>e</sup> | 2                              | yes           | chromosome                             |
| 72554   | 107.564              | 42.227              | 11                             | 2,988,108             | 2  | 2,988,108;<br>1,171,702                      | 3   | 156,00 <sup>d</sup> ;<br>8,970 <sup>e</sup> ;<br>7,703 <sup>e</sup>    | 6                              | yes           | chromosome                             |
| 71813   | 125.569              | 311.889             | 6                              | 3,902,837             | 2  | 3,902,837;<br>34,129                         | 1   | 14,782   | 3                              | yes           | chromosome                             |
| 67098   | 121.990              | 129.754             | 2                              | 4,073,402             | 1  | 4,073,402                                    | 1   | 16,673   | 0                              | yes           | chromosome                             |
| MC1     | 84.566               | 278.578             | 3                              | 4,026,212             | 1  | 4,026,212                                    | 2   | 184,748;<br>8,731  | 0                              | yes           | chromosome                             |

<sup>a</sup> Based on hybrid assembly using Unicycler.

<sup>b</sup> Based on the gene content identified with genome annotation.

<sup>c</sup> All undefined contigs are <5 kbp.

<sup>d</sup> >90% sequence similarity and coverage with the 184 kbp plasmid from MC1.

<sup>e</sup> >99% sequence similarity and coverage with the 16 kbp plasmid from 67098.